

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/524/295  
Source: PCT  
Date Processed by STIC: 1-24-06

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PCT

## RAW SEQUENCE LISTING

DATE: 01/24/2006

PATENT APPLICATION: US/10/524,295

TIME: 10:24:58

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\01052006\J524295.raw

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5 <110> APPLICANT: TransMIT Gesellschaft for Technologietransfer mbH
7      TransMIT Gesellschaft for Technologietransfer mbH
11 <120> TITLE OF INVENTION: Method for screening the allelic state at the 5'-flanking
region of the
12      aS1 casein gene
16 <130> FILE REFERENCE: An127/Pri
C--> 20 <140> CURRENT APPLICATION NUMBER: US/10/524,295
C--> 22 <141> CURRENT FILING DATE: 2005-02-11
26 <150> PRIOR APPLICATION NUMBER: DE 102 38 433 A1
28 <151> PRIOR FILING DATE: 2002-08-16
32 <160> NUMBER OF SEQ ID NOS: 8
36 <170> SOFTWARE: PatentIn version 3.1
40 <210> SEQ ID NO: 1
42 <211> LENGTH: 18
44 <212> TYPE: DNA
46 <213> ORGANISM: Bos spec.
50 <220> FEATURE:
W--> 52 <221> NAME/KEY: Primer 2
54 <222> LOCATION: (1)..(18)
56 <223> OTHER INFORMATION: 18 basepair, single stranded nucleic acid (linear)
60 <400> SEQUENCE: 1
61 gaagaagcag caagctgg                                     18
64 <210> SEQ ID NO: 2
66 <211> LENGTH: 19
68 <212> TYPE: DNA
70 <213> ORGANISM: Bos spec.
74 <220> FEATURE:
W--> 76 <221> NAME/KEY: Primer 3
78 <222> LOCATION: (1)..(19)
80 <223> OTHER INFORMATION: 19 basepair, single stranded nucleic acid (linear)
84 <400> SEQUENCE: 2
85 ccttgaaata ttctaccag                                     19
88 <210> SEQ ID NO: 3
90 <211> LENGTH: 1061
92 <212> TYPE: DNA
94 <213> ORGANISM: Bos taurus
98 <220> FEATURE:
W--> 100 <221> NAME/KEY: alpha-S1Kaseingen
102 <222> LOCATION: (1)..(1061)
104 <223> OTHER INFORMATION: start Exon 1 at position 620
108 <300> PUBLICATION INFORMATION:
110 <301> AUTHORS: Koczan Dirk, Hobom Gerd, Seyfert Hans-Martin
112 <302> TITLE: Genomic organization of the bovine alpha S1-casein gene
114 <303> JOURNAL: Nucleic acids research

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116 <304> VOLUME: 19
118 <305> ISSUE: 20
120 <306> PAGES: 5591
122 <307> DATE: 1991-09-24
124 <308> DATABASE ACCESSION NO: X59856
126 <309> DATABASE ENTRY DATE: 1991-07-18
128 <313> RELEVANT RESIDUES: (1)..(1061)
132 <300> PUBLICATION INFORMATION:
134 <308> DATABASE ACCESSION NO: EMBL X59856
136 <309> DATABASE ENTRY DATE: 1991-07-18
138 <313> RELEVANT RESIDUES: (1)..(1061)
142 <400> SEQUENCE: 3
143 gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg      60
145 gtataattaa aatgccacca aaattttata aataattata ttttcttttt gcaggaaaaa      120
147 gattagacca catataatgt aactttatttc acaaggtaaa taattataat aaataatatg      180
149 gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatggt      240
151 aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacagggtat      300
153 tgaatttttc aaagggttaca aaggaaattt tattgatata ataaatgcat gttctcataa      360
155 taaccataaa tctagggttt tgttggggtt tttttttggt tgttaattta gaacaatgcc      420
157 attccatttc ctgtataatg agtcacttct ttgttgtaaa ctctccttag aatttcttgg      480
159 gagaggaact gaacagaaca ttgatttctt atgtgagaga attcttagaa tttaaataaa      540
161 cctgttggtt aaactgaaac cacaaaatta gcattttact aatcagtagg tttaaatagc      600
163 ttggaagcaa aagtctgcca tcaccttgat catcaaccca gcttgctgct tcttcccagt      660
165 cttgggttca aggtattatg tatacatata acaaaatttc tatgattttc ctctgtctca      720
167 tctttcattc ttcactaata cgcagttgta acttttctat gtgattgcaa gtattggtac      780
169 tttcctatga tatactgtta gcttaaaaaat atatttgcaa atggtgatac tatctatctc      840
171 agagctatag gtgaaaaatt aaatactttt ataaagacca aattgatcat ttttaaacga      900
173 aattcttata tactgaaaat gtagatacat aacttcagta tagatttatg gtaaaataat      960
175 ttgaatcatt tttgtcaaat tctgtaaaaa gttgtcatac agaataattt ataataattt      1020
177 tgttttcata gaaataacat ttctggtaga atatttcaag g                                1061

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180 &lt;210&gt; SEQ ID NO: 4

182 &lt;211&gt; LENGTH: 652

184 &lt;212&gt; TYPE: DNA

186 &lt;213&gt; ORGANISM: Bos taurus

190 &lt;220&gt; FEATURE:

W--> 192 <221> NAME/KEY: CSN1S1-gene, 5'flanking region from position 616 and Exon 1 at position

W--> 193 617

195 &lt;222&gt; LOCATION: (1)..(652)

197 <223> OTHER INFORMATION: Mutation/SNP position 83 (A to G), position 98 (A to G), position

198 298 (A to C), position 442 (A to G; change/loss of YY1- and AP1

199 -bindingsite), position 541 (G to A);

200 deletion TT between position 389 and 394 compaired with Allel2

204 &lt;400&gt; SEQUENCE: 4

```

205 gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg      60
207 gtataattaa aatgccacca aagttttata aataattgta ttttcttttt gcaggaaaaa      120
209 gattagacca catataatgt aactttatttc acaaggtaaa taattataat aaataatatg      180
211 gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatggt      240
213 aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttctt ttacagggtat      300
215 tgaatttttc aaagggttaca aaggaaattt tattgatata ataaatgcat gttctcataa      360

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217 taaccataaa tctaggggtt tgttgggggt ttttgtttgt taatttagaa caatgccatt      420
219 ccatttcctg tataatgagt cgcttctttg ttgtaaactc tccttagaat ttcttgggag      480
221 aggaactgaa cagaacattg atttcctatg tgagagaatt cttagaattt aaataaacct      540
223 attggttaaa ctgaaaccac aaaattagca ttttactaat cagtagggtt aaatagcttg      600
225 gaagcaaaag tctgccatca ccttgatcat caaccagct  tgctgctttc tt              652
228 <210> SEQ ID NO: 5
230 <211> LENGTH: 654
232 <212> TYPE: DNA
234 <213> ORGANISM: Bos taurus
238 <220> FEATURE:
W--> 240 <221> NAME/KEY: CSN1S1-gene, 5`flanking region and Exon 1
242 <222> LOCATION: (1)..(654)
244 <223> OTHER INFORMATION: Bindingsite for transcriptionfactor AP-1 at position 438 to
445
245      Bindingsite for transcriptionfactor YY-1 at position 443 to 448
249 <400> SEQUENCE: 5
250 gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg      60
252 gtataattaa aatgccacca aaatttatac aataattata ttttcttttt gcaggaaaaa      120
254 gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataaatatg      180
256 gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatggt      240
258 aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacaggtat      300
260 tgaatttttc aaagggttaca aaggaaattt tattgatata ataaatgcat gttctcataa      360
262 taaccataaa tctaggggtt tgttgggggt tttttgttt gttaatttag aacaatgcca      420
264 ttccatttcc tgtataatga gtcacttctt tgttgtaaac tctccttaga atttcttggg      480
266 agaggaactg aacagaacat tgatttcccta tgtgagagaa ttcttagaat ttaaataaac      540
268 ctggttggtta aactgaaacc acaaaattag cattttacta atcagtaggt ttaaataagct      600
270 tggaaagcaa agtctgccat caccttgatc atcaaccagc cttgctgctt tctt              654
273 <210> SEQ ID NO: 6
275 <211> LENGTH: 650
277 <212> TYPE: DNA
279 <213> ORGANISM: Bos taurus
283 <220> FEATURE:
W--> 285 <221> NAME/KEY: CSN1S1-gene, 5`flanking region
287 <222> LOCATION: (1)..(650)
289 <223> OTHER INFORMATION: Bindingsite for transcriptionfactor AP-1 at position 434 to
441
290      Bindingsite for transcriptionfactor YY-1 at position 439 to 444
291      deletion G and TTT between 390 and 396 compaired with Allel 2
295 <400> SEQUENCE: 6
296 gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg      60
298 gtataattaa aatgccacca aaatttatac aataattata ttttcttttt gcaggaaaaa      120
300 gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataaatatg      180
302 gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatggt      240
304 aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacaggtat      300
306 tgaatttttc aaagggttaca aaggaaattt tattgatata ataaatgcat gttctcataa      360
308 taaccataaa tctaggggtt tgttgggggt tttttgttta atttagaaca atgccattcc      420
310 atttctgtga taatgagtca cttctttgtt gtaaactctc cttagaattt cttgggagag      480
312 gaactgaaca gaacattgat ttctatgtg agagaattct tagaatttaa ataaacctgt      540
314 tggttaaact gaaaccacaa aattagcatt ttactaatca gtaggtttaa atagcttgga      600
316 agcaaaagtc tgccatcacc ttgatcatca acccagcttg ctgctttctt              650
319 <210> SEQ ID NO: 7

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TIME: 10:24:58

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\01052006\J524295.raw

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321 <211> LENGTH: 650
323 <212> TYPE: DNA
325 <213> ORGANISM: Bos taurus
329 <220> FEATURE:
W--> 331 <221> NAME/KEY: CSN1S1-gene, 5`flanking region
333 <222> LOCATION: (1)..(650)
335 <223> OTHER INFORMATION: Bindingsite for transcriptionfactors: AP-1 at position 434
to 441
336      , ABF1 at position 469 to 483, YY-1 at position 439 to 444;
337      mutation (SNP) at position 480 (G to C), developing a ABF1-bindin
338      gsite;
W--> 339      deletion G and TTT between position 390 and 396 compaired with A1
W--> 340      lel 2
344 <400> SEQUENCE: 7
345 gaatgaatga actagttacc acaactagta caccacaaat gaacacaaaa tagcttggtg      60
347 gtataattaa aatgccacca aaattttatac aataattata tttctttttt gcaggaaaaa      120
349 gattagacca catataatgt aactttatttc acaaggtaaa taattataat aaataatatg      180
351 gattaactga gtttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatggt      240
353 aataaaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacagggtat      300
355 tgaatttttc aaagggttaca aaggaaattt tattgatata ataaatgcat gttctcataa      360
357 taaccataaa tctagggttt tggtgggggtt ttttttgta atttagaaca atgccattcc      420
359 atttcctgta taatgagtca cttctttggt gtaaactctc cttagaattt cttgggagac      480
361 gaactgaaca gaacattgat ttcctatgtg agagaattct tagaatttaa ataaacctgt      540
363 tgggttaaaact gaaaccacaa aattagcatt ttactaatca gtaggtttaa atagcttgga      600
365 agcaaaaagtc tgccatcacc ttgatcatca acccagcttg ctgctttctt      650
368 <210> SEQ ID NO: 8
370 <211> LENGTH: 20
372 <212> TYPE: DNA
374 <213> ORGANISM: Bos spec.
378 <220> FEATURE:
W--> 380 <221> NAME/KEY: Primer1
382 <222> LOCATION: (1)..(20)
384 <223> OTHER INFORMATION: 20 basepair, single stranded nucleic acid (linear)
388 <400> SEQUENCE: 8
389 gaatgaatga actagttacc      20

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**VERIFICATION SUMMARY**

DATE: 01/24/2006

PATENT APPLICATION: US/10/524,295

TIME: 10:24:59

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\01052006\J524295.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:52 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:76 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
L:100 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:192 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:193 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:4  
L:240 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:285 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:331 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:339 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:340 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:380 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8